



2590  
1113

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/620,955A

Source: DIP

Date Processed by STIC: 11/16/01

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 091620, 955A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4      Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                                   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   (i)       SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   This sequence is intentionally skipped  
  
                                   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                                   <210> sequence id number  
                                   <400> sequence id number  
                                   000
  
- 9 ✓      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                                   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                                   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                                   Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 06/04/2001

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## RAW SEQUENCE LISTING

DATE: 11/16/2001

PATENT APPLICATION: US/09/620,955A

TIME: 10:27:12

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11162001\I620955A.raw

**Does Not Comply  
Corrected Diskette Needed**

3 <110> APPLICANT: Huston, James s  
 4 Messer, Anne  
 5 Lecerf, Jean-Michel  
 7 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE  
 8 ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS  
 10 <130> FILE REFERENCE: INR-004CP  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/620,955A  
 C--> 13 <141> CURRENT FILING DATE: 2000-07-21  
 15 <150> PRIOR APPLICATION NUMBER: 60/146,047  
 16 <151> PRIOR FILING DATE: 1999-07-27  
 18 <160> NUMBER OF SEQ ID NOS: 45  
 20 <170> SOFTWARE: PatentIn Ver. 2.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 345  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Artificial Sequence  
 27 <220> FEATURE:  
 28 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 29 construct  
 31 <220> FEATURE:  
 32 <223> OTHER INFORMATION: The VH sequence uses a V segment of the VH3  
 33 family.  
 35 <220> FEATURE:  
 36 <223> OTHER INFORMATION: CDR1 sequence: from base 91 to base 105 (15  
 37 bases).  
 39 <220> FEATURE:  
 40 <223> OTHER INFORMATION: CDR2 sequence: from base 148 to base 198 (51  
 41 bases).  
 43 <220> FEATURE:  
 44 <223> OTHER INFORMATION: CDR3 sequence: from base 295 to base 312 (18  
 45 bases).  
 47 <400> SEQUENCE: 1  
 48 caggtgcagc tgcaggagtc ggggggaggc ttggtacagc ctgggggggtc cctgagactc 60  
 49 tcctgtgcag cctctggatt caccttcagt agttatagca tgagctgggt ccgccaggct 120  
 50 ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagcaa taaatactac 180  
 51 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240  
 52 cttcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatagg 300  
 53 tacttcgatc tctggggccg tggcaccctg gtcaccgtct cctca 345  
 55 <210> SEQ ID NO: 2  
 56 <211> LENGTH: 115  
 57 <212> TYPE: PRT  
 58 <213> ORGANISM: Artificial Sequence  
 60 <220> FEATURE:  
 61 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 62 construct  
 64 <400> SEQUENCE: 2  
 65 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

*Errors on pp. 5*

→ The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

## RAW SEQUENCE LISTING

DATE: 11/16/2001

PATENT APPLICATION: US/09/620,955A

TIME: 10:27:12

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11162001\I620955A.raw

```

66      1              5              10              15
68 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
69              20              25              30
71 Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
72              35              40              45
74 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
75              50              55              60
77 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
78      65              70              75              80
80 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
81              85              90              95
83 Ala Arg Asp Arg Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr
84              100              105              110
86 Val Ser Ser
87      115
90 <210> SEQ ID NO: 3
91 <211> LENGTH: 327
92 <212> TYPE: DNA
93 <213> ORGANISM: Artificial Sequence
95 <220> FEATURE:
96 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
97      construct
99 <220> FEATURE:
100 <223> OTHER INFORMATION: The VL sequence uses a V segment of the VL2
101      family.
103 <220> FEATURE:
104 <223> OTHER INFORMATION: CDR1 sequence: from base 67 to base 108 (42
105      bases).
107 <220> FEATURE:
108 <223> OTHER INFORMATION: CDR2 sequence: from base 154 to base 174 (21
109      bases).
111 <220> FEATURE:
112 <223> OTHER INFORMATION: CDR3 sequence: from base 271 to base 294 (24
113      bases).
115 <400> SEQUENCE: 3
116 cagtctgccc tgactcagcc tgccctcogtg tctgggtctc ctggacagtc gatcaccatc 60
117 tcctgcactg gaaccagcag tgacattggt gcttataact atgtctcctg gtaccagcag 120
118 tatccaggca aggcccccaa actccttatt tatgatgtca gtaatcggcc ctcagggatt 180
119 tctaatcgct tctctggctc caagtctggc gatacggcct cctgaccat ctctgggctc 240
120 caggctgagg acgaggctga ttattactgc agctcatttg cgaacagcgg ccccttattc 300
121 ggcggaggga ccaaggtcac cgtccta 327
123 <210> SEQ ID NO: 4
124 <211> LENGTH: 109
125 <212> TYPE: PRT
126 <213> ORGANISM: Artificial Sequence
128 <220> FEATURE:
129 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
130      construct
132 <400> SEQUENCE: 4

```

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## RAW SEQUENCE LISTING

DATE: 11/16/2001

PATENT APPLICATION: US/09/620,955A

TIME: 10:27:12

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11162001\I620955A.raw

```

133 Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
134   1           5           10           15
136 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Ile Gly Ala Tyr
137           20           25           30
139 Asn Tyr Val Ser Trp Tyr Gln Gln Tyr Pro Gly Lys Ala Pro Lys Leu
140           35           40           45
142 Leu Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Ile Ser Asn Arg Phe
143           50           55           60
145 Ser Gly Ser Lys Ser Gly Asp Thr Ala Ser Leu Thr Ile Ser Gly Leu
146           65           70           75           80
148 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Phe Ala Asn Ser
149           85           90           95
151 Gly Pro Leu Phe Gly Gly Gly Thr Lys Val Thr Val Leu
152           100          105
155 <210> SEQ ID NO: 5
156 <211> LENGTH: 717
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
162   construct
164 <400> SEQUENCE: 5
165 caggtgcagc tgcaggagtc ggggggaggc ttggtacagc ctgggggggc cctgagactc 60
166 tcctgtgcag cctctggatt caccttcagt agttatagca tgagctgggt ccgccaggct 120
167 ccaggcaagg ggtctggagt ggtggcagtt atatcatatg atggaagcaa taaatactac 180
168 gcagactccg tgaaggggcg attcaccatc tccagagaca attccaagaa cacgctgtat 240
169 cttcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagagatagg 300
170 tacttcgata tctggggccg tggcaccctg gtcaccgtct cctcagggtg aggcggttca 360
171 ggcggagggt gctctggcgg tggcggatcg cagtctgccc tgactcagcc tgctctcgtg 420
172 tctgggtctc ctggacagtc gatcaccatc tctgcactg gaaccagcag tgacattggt 480
173 gcttataact atgtctcctg gtaccagcag tatccaggca agggccccaactccttatt 540
174 tatgatgtca gtaatcggcc ctcagggtatt tctaatecgt tctctggctc caagtctggc 600
175 gatacggcct ccctgaccat ctctgggctc caggctgagg acgaggctga ttattactgc 660
176 agctcatttg cgaacagcgg ccccttattc ggcggaggga ccaaggtcac cgtccta 717
178 <210> SEQ ID NO: 6
179 <211> LENGTH: 239
180 <212> TYPE: PRT
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
185   construct
187 <400> SEQUENCE: 6
188 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
189   1           5           10           15
191 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
192           20           25           30
194 Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
195           35           40           45
197 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val

```

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PATENT APPLICATION: US/09/620,955A

TIME: 10:27:12

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11162001\I620955A.raw

```

198      50      55      60
200 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
201 65      70      75      80
203 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
204      85      90      95
206 Ala Arg Asp Arg Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr
207      100      105      110
209 Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
210      115      120      125
212 Gly Ser Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro
213      130      135      140
215 Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Ile Gly
216 145      150      155      160
218 Ala Tyr Asn Tyr Val Ser Trp Tyr Gln Gln Tyr Pro Gly Lys Ala Pro
219      165      170      175
221 Lys Leu Leu Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Ile Ser Asn
222      180      185      190
224 Arg Phe Ser Gly Ser Lys Ser Gly Asp Thr Ala Ser Leu Thr Ile Ser
225      195      200      205
227 Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Phe Ala
228      210      215      220
230 Asn Ser Gly Pro Leu Phe Gly Gly Gly Thr Lys Val Thr Val Leu
231 225      230      235
234 <210> SEQ ID NO: 7
235 <211> LENGTH: 44
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
241 construct
243 <400> SEQUENCE: 7
244 tcaccgtctc ctcaggtgga ggcggttcag gcggaggtgg ctct 44
246 <210> SEQ ID NO: 8
247 <211> LENGTH: 48
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
253 construct
255 <400> SEQUENCE: 8
256 tgggtgagct catgtccgmt ccgccaccgc cagagccacc tccgcctg 48
258 <210> SEQ ID NO: 9
259 <211> LENGTH: 35
260 <212> TYPE: PRT
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
265 construct
267 <220> FEATURE:

```

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## RAW SEQUENCE LISTING

DATE: 11/16/2001

PATENT APPLICATION: US/09/620,955A

TIME: 10:27:12

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11162001\I620955A.raw

*Must give location of Xaa, see error summary sheet, item 9*

268 <223> OTHER INFORMATION: where X represents 35 glutamine (Q) residues  
 270 <400> SEQUENCE: 9

W--> 271 Leu Val Pro Arg Gly Ser Val Ser Thr His His His His Xaa His  
 272 1 5 10 15  
 274 His Gly Asn Ser Gly Pro Pro Glu Phe Pro Gly Arg Leu Glu Arg Pro  
 275 20 25 30  
 277 His Arg Asp  
 278 35

281 <210> SEQ ID NO: 10  
 282 <211> LENGTH: 35  
 283 <212> TYPE: PRT  
 284 <213> ORGANISM: Artificial Sequence  
 286 <220> FEATURE:  
 287 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 288 construct  
 290 <220> FEATURE: *same error*

291 <223> OTHER INFORMATION: where X represents 25 glutamine (Q) residues  
 293 <400> SEQUENCE: 10

294 Leu Val Pro Arg Gly Ser Met Ala Thr Leu Glu Lys Leu Met Lys Ala  
 295 1 5 10 15

W--> 297 Phe Glu Ser Leu Lys Ser Phe Xaa Leu Gln Pro Gly Ser Thr Arg Ala  
 298 20 25 30  
 300 Ala Ala Ser  
 301 35

304 <210> SEQ ID NO: 11  
 305 <211> LENGTH: 34  
 306 <212> TYPE: PRT  
 307 <213> ORGANISM: Artificial Sequence  
 309 <220> FEATURE:  
 310 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 311 construct  
 313 <220> FEATURE:

314 <223> OTHER INFORMATION: where X represents 42 glutamine (Q) residues  
 316 <400> SEQUENCE: 11

317 Leu Val Pro Arg Gly Ser Met Ala Thr Leu Glu Lys Leu Met Lys Ala  
 318 1 5 10 15  
 320 Phe Glu Ser Leu Lys Ser Phe Leu Gln Pro Gly Ser Thr Arg Ala Ala  
 321 20 25 30  
 323 Ala Ser

327 <210> SEQ ID NO: 12  
 328 <211> LENGTH: 18  
 329 <212> TYPE: PRT  
 330 <213> ORGANISM: Artificial Sequence  
 332 <220> FEATURE:  
 333 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 334 construct  
 336 <220> FEATURE:  
 337 <223> OTHER INFORMATION: where X represents 47 glutamine (Q) residues  
 339 <400> SEQUENCE: 12

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## VERIFICATION SUMMARY

DATE: 11/16/2001

PATENT APPLICATION: US/09/620,955A

TIME: 10:27:13

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11162001\I620955A.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:271 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9  
L:271 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9  
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:297 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:297 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:343 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12  
L:343 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12  
L:343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:363 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13  
L:363 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13  
L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:383 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14  
L:383 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14  
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:403 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15  
L:403 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15  
L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:429 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16  
L:429 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16  
L:429 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:455 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17  
L:455 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17  
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:484 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18  
L:484 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18  
L:484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:507 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19  
L:507 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19  
L:507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:527 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20  
L:527 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20  
L:527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20

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